



SEQUENCE LISTING

Box Sequence  
08 447118

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Burkly, Linda C.  
(B) STREET: 34 Winthrop Street  
(C) CITY: West Newton  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) POSTAL CODE (ZIP): 02165

(A) NAME: Biogen, Inc.  
(B) STREET: Fourteen Cambridge Center  
(C) CITY: Cambridge  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) POSTAL CODE (ZIP): 02142

(ii) TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES

(iii) NUMBER OF SEQUENCES: 15

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 000000 (BGP-151CP)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/01456  
(B) FILING DATE: 09-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/029,330  
(B) FILING DATE: 09-FEB-1993

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..360

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1

(D) OTHER INFORMATION:/note= "pBAG159 insert: HP1/2 heavy chain variable region; amino acid 1 is Glu (E) but Gln(Q) may be substituted"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA	48
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser	
1 5 10 15	
GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT	96
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr	
20 25 30	
ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA	144
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly	
35 40 45	
AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG	192
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln	
50 55 60	
GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG	240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu	
65 70 75 80	
CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA	288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA	336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln	
100 105 110	
GGG ACC ACG GTC ACC GTC TCC TCA	360
Gly Thr Thr Val Thr Val Ser Ser	
115 120	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser	
1 5 10 15	
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr	
20 25 30	
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly	
35 40 45	

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln  
50 55 60

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu  
65 70 75 80

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln  
100 105 110

Gly Thr Thr Val Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION:/product= "HP1/2 light chain variable region"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "pBAG172 insert: HP1/2 light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA	48
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly	
125 130 135	
GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT	96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp	
140 145 150	
GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA	144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
155 160 165	
TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC	192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
170 175 180	
AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT	240

Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala	
185					190					195					200	
GAA	GAC	CTG	GCA	GTT	TAT	TTC	TGT	CAG	CAG	GAT	TAT	AGC	TCT	CCG	TAC	288
Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr	
				205					210					215		
ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAG	ATC							318
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
			220					225								

(2) INFORMATION FOR SEO ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp
			20					25					30		
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
	50					55					60				
Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala
65					70					75					80
Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile						
			100					105							

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..429

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..57

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 58..429

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION:/note= "pBAG195 insert: AS heavy chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT	48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly	
-19 -15 -10 -5	
GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA	96
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
1 5 10	
CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GCG TCT GGC TTC AAC ATT	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile	
15 20 25	
AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT	192
Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu	
30 35 40 45	
GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC	240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp	
50 55 60	
CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AGC AAC	288
Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn	
65 70 75	
CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
80 85 90	
TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC	384
Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp	
95 100 105	
TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC	429
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser	
110 115 120	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-19          -15          -10          -5

Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
      1              5              10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
    15              20              25

Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
    30              35              40              45

Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
      50              55              60

Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
      65              70              75

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
    80              85              90

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
    95              100             105

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110              115              120
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..386

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..57

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 58..386

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1

(D) OTHER INFORMATION:/note= "pBAG198 insert: VK2  
(SVMDY) light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val	
15 20 25	
ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG	192
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40 45	
CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA	240
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg	
50 55 60	
TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser	
80 85 90	
TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG	384
Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys	
95 100 105	
TG	386

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
1 5 10	

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val  
 15 20 25  
 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
 30 35 40 45  
 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg  
 50 55 60  
 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
 65 70 75  
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser  
 80 85 90  
 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys  
 95 100 105

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1338

(ix) FEATURE:

- (A) NAME/KEY: VCAM-1 gene segment
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861(1991).

(ix) FEATURE:

- (A) NAME/KEY: Hinge region
- (B) LOCATION: 220..229
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the hinge region of Human IgG1 heavy chain constant region.

(ix) FEATURE:

- (A) NAME/KEY: Heavy chain constant region 2
- (B) LOCATION: 230..338
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 2 of Human IgG1 heavy chain constant region.



(ix) FEATURE:

(A) NAME/KEY: Heavy chain constant region 3

(B) LOCATION: 339..446

(D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 3 of Human IgG1 heavy chain constant region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG CCT GGG AAG ATG GTC GTG ATC CTT GGA GCC TCA AAT ATA CTT TGG	48
Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp	
110 115 120 125	
ATA ATG TTT GCA GCT TCT CAA GCT TTT AAA ATC GAG ACC ACC CCA GAA	96
Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu	
130 135 140	
TCT AGA TAT CTT GCT CAG ATT GGT GAC TCC GTC TCA TTG ACT TGC AGC	144
Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser	
145 150 155	
ACC ACA GGC TGT GAG TCC CCA TTT TTC TCT TGG AGA ACC CAG ATA GAT	192
Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp	
160 165 170	
AGT CCA CTG AAT GGG AAG GTG ACG AAT GAG GGG ACC ACA TCT ACG CTG	240
Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu	
175 180 185	
ACA ATG AAT CCT GTT AGT TTT GGG AAC GAA CAC TCT TAC CTG TGC ACA	288
Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr	
190 195 200 205	
GCA ACT TGT GAA TCT AGG AAA TTG GAA AAA GGA ATC CAG GTG GAG ATC	336
Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile	
210 215 220	
TAC TCT TTT CCT AAG GAT CCA GAG ATT CAT TTG AGT GGC CCT CTG GAG	384
Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu	
225 230 235	
GCT GGG AAG CCG ATC ACA GTC AAG TGT TCA GTT GCT GAT GTA TAC CCA	432
Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro	
240 245 250	
TTT GAC AGG CTG GAG ATA GAC TTA CTG AAA GGA GAT CAT CTC ATG AAG	480
Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys	
255 260 265	
AGT CAG GAA TTT CTG GAG GAT GCA GAC AGG AAG TCC CTG GAA ACC AAG	528
Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys	
270 275 280 285	
AGT TTG GAA GTA ACC TTT ACT CCT GTC ATT GAG GAT ATT GGA AAA GTT	576
Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val	
290 295 300	

CTT GTT TGC CGA GCT AAA TTA CAC ATT GAT GAA ATG GAT TCT GTG CCC	624
Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro	
305 310 315	
ACA GTA AGG CAG GCT GTA AAA GAA TTG CAA GTC GAC AAA ACT CAC ACA	672
Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr	
320 325 330	
TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC	720
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe	
335 340 345	
CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT	768
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro	
350 355 360 365	
GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC	816
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val	
370 375 380	
AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA	864
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr	
385 390 395	
AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC	912
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val	
400 405 410	
CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC	960
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys	
415 420 425	
AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC	1008
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser	
430 435 440 445	
AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA	1056
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro	
450 455 460	
TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC	1104
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val	
465 470 475	
AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG	1152
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly	
480 485 490	
CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC	1200
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp	
495 500 505	
GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG	1248
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp	
510 515 520 525	
CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC	1296

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His	
530 535 540	
AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA	1338
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
545 550 555	
TGAGTGCGG	1347

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 6..23
  - (D) OTHER INFORMATION: This corresponds to Kinase  
Primer 370-31.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TCGTC GAC AAA ACT CAC ACA TGC C	24
Asp Lys Thr His Thr Cys	
1 5	

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (D) OTHER INFORMATION: This corresponds to Kinase  
Primer 370-32.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTAAATGAGT GCGGCGGCCG CCAA	24
----------------------------	----

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCGGCCGCGG TCCAACCACC AATCTCAAAG CTTGGTACCC GGGAATTCAG ATCTGCAGCA	60
TGCTCGAGCT CTAGATATCG ATTCCATGGA TCCTCACATC CCAATCCGCG GCCGC	115

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 21..41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GAGCTCGAGG CGGCCGCACC ATG CCT GGG AAG ATG GTC GTG	41
Met Pro Gly Lys Met Val Val	
1 5	

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAGTCGACTT GCAATTCTTT TAC

23

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCGACGCGGC CGCG

14